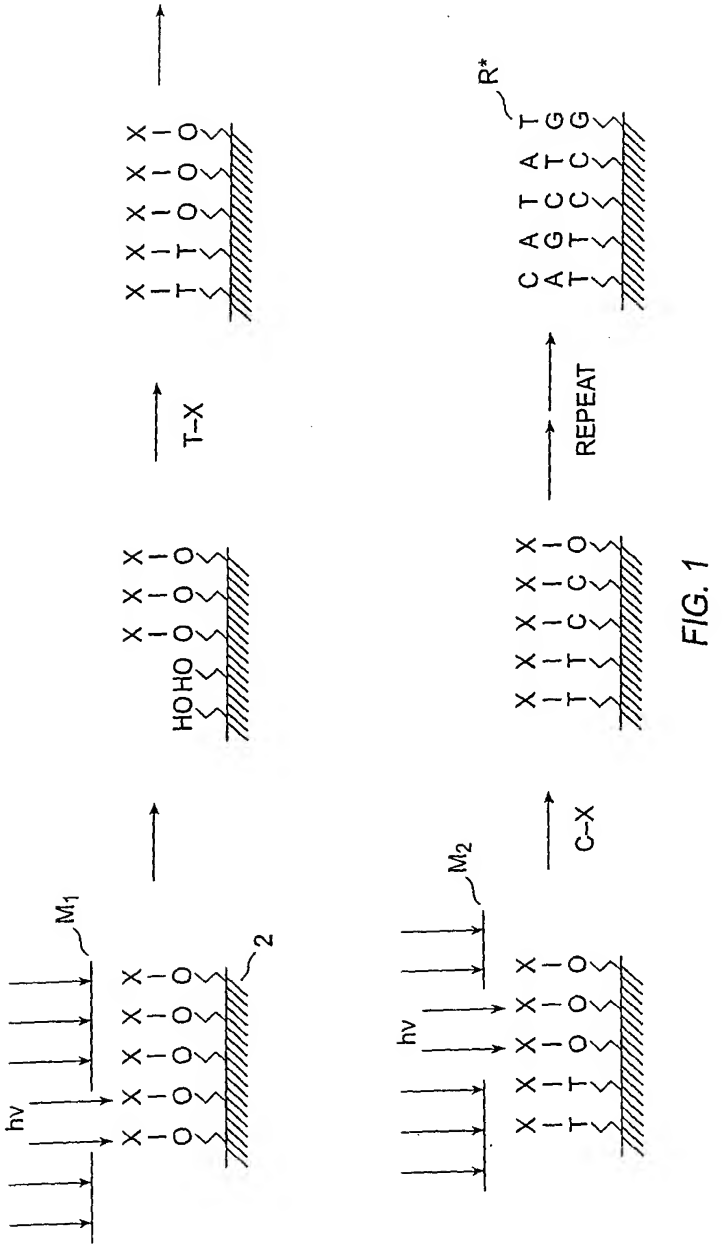


FIG. 1

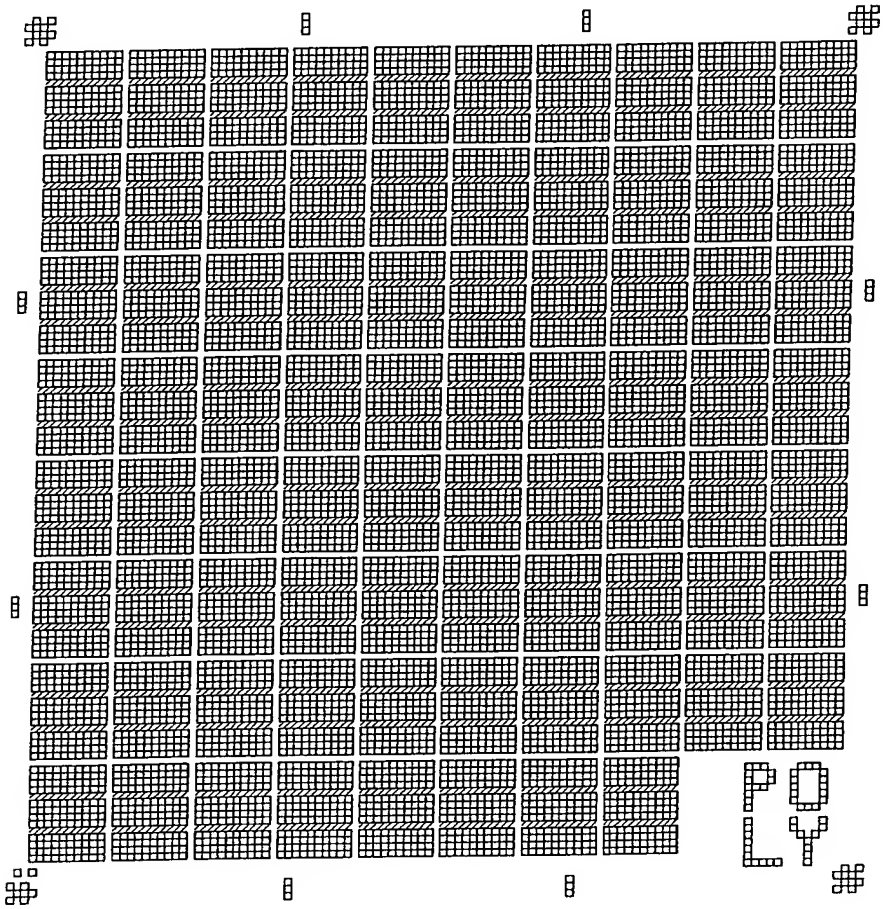
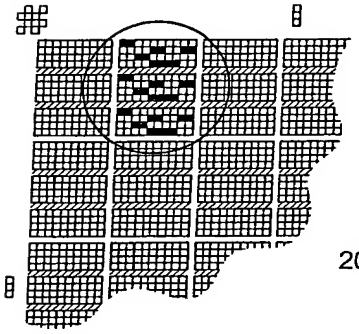


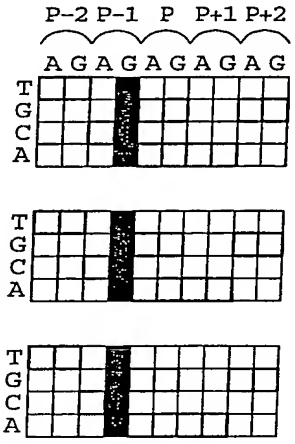
FIG. 2A



SEQUENCE AT POLYMORPHISM WI-567

5' 3'
TGCTGCCTTGGTTC [A/G] AGCCCTCATCTCTTT

THREE BLOCKS OF COMPLEMENTARY
20-MER OLIGOS WITH SUBSTITUTIONS (**N**)
7, 10 AND 13 BP FROM THE 3' END



BASES IN THE SHADED COLUMNS

3' BLOCK 20/7 5'
AACCAAN [C] TCGGGAGTAGAG

3' BLOCK 20/10 5'
CGGAACCAAN [C] TCGGGAGTA

3' BLOCK 20/13 5'
CGACGGAACCAAN [C] TCGGGA

FIG. 2B

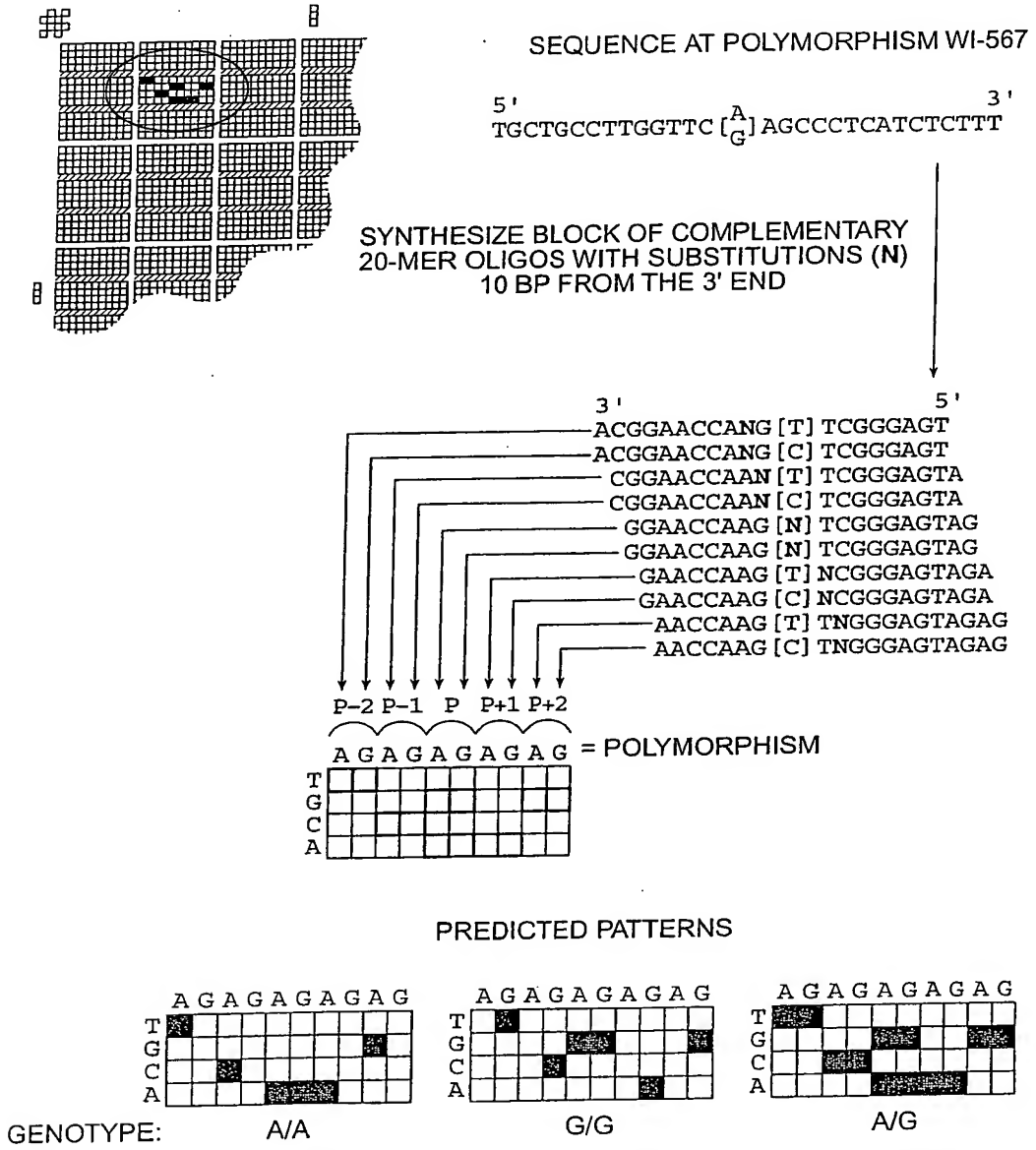

SEQUENCE AT POLYMORPHISM WI-567
5' 3'
TGCTGCCTTGGTTC [A/G] AGCCCTCATCTCTTT
SYNTHESIZE BLOCK OF COMPLEMENTARY
20-MER OLIGOS WITH SUBSTITUTIONS (N)
10 BP FROM THE 3' END
3' 5'
ACGGAACCANG [T] TCGGGAGT
ACGGAACCANG [C] TCGGGAGT
CGGAACCAAN [T] TCGGGAGTA
CGGAACCAAN [C] TCGGGAGTA
GGAACCAAG [N] TCGGGAGTAG
GGAACCAAG [N] TCGGGAGTAG
GAACCAAG [T] NCGGGAGTAGA
GAACCAAG [C] NCGGGAGTAGA
AACCAAG [T] TNGGGAGTAGAG
AACCAAG [C] TNGGGAGTAGAG
P-2 P-1 P P+1 P+2
A G A G A G A G A G = POLYMORPHISM
T
G
C
A
PREDICTED PATTERNS
A G A G A G A G A G
T
G
C
A
GENOTYPE:
A/A
G/G
A/G

FIG. 3

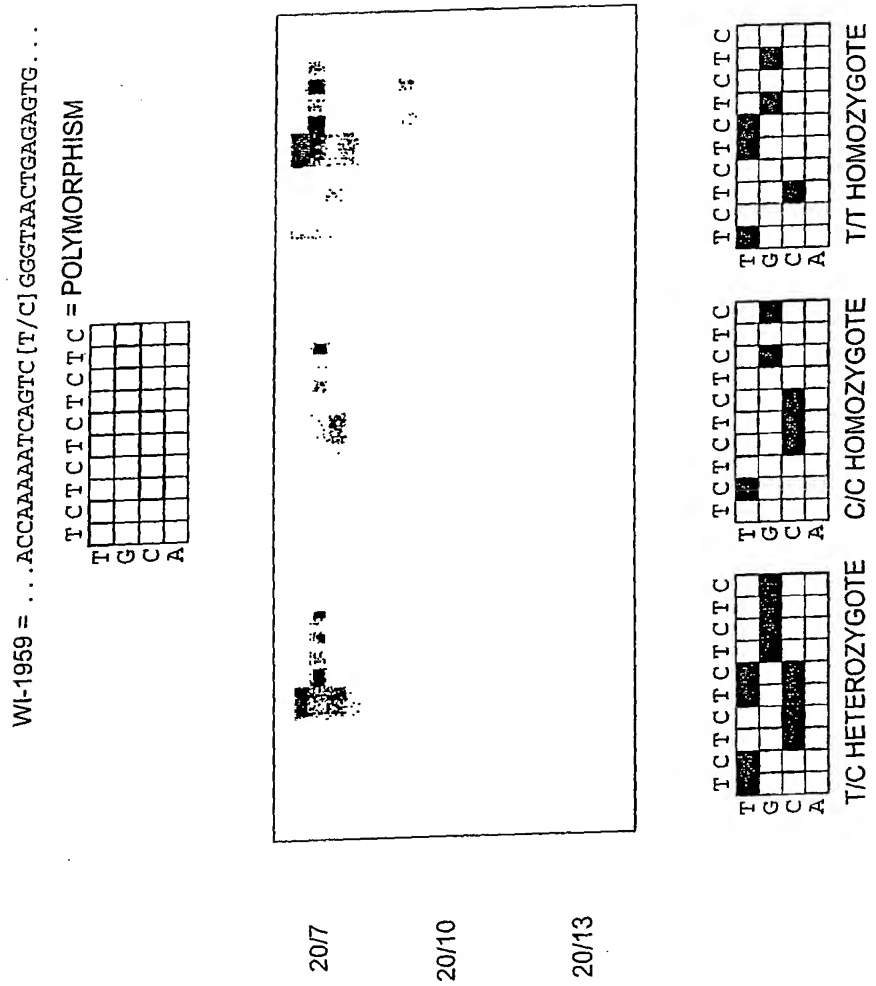

WI-1959 = . . .ACCAAAAATCAGTC [T/C] GGGTAACTGAGAGTG. . .
T C T C T C T C T C = POLYMORPHISM
T
G
C
A
20/7
20/10
20/13
T C T C T C T C T C
T/C HETEROZYGOTE
C/C HOMOZYGOTE
T/T HOMOZYGOTE

FIG. 4

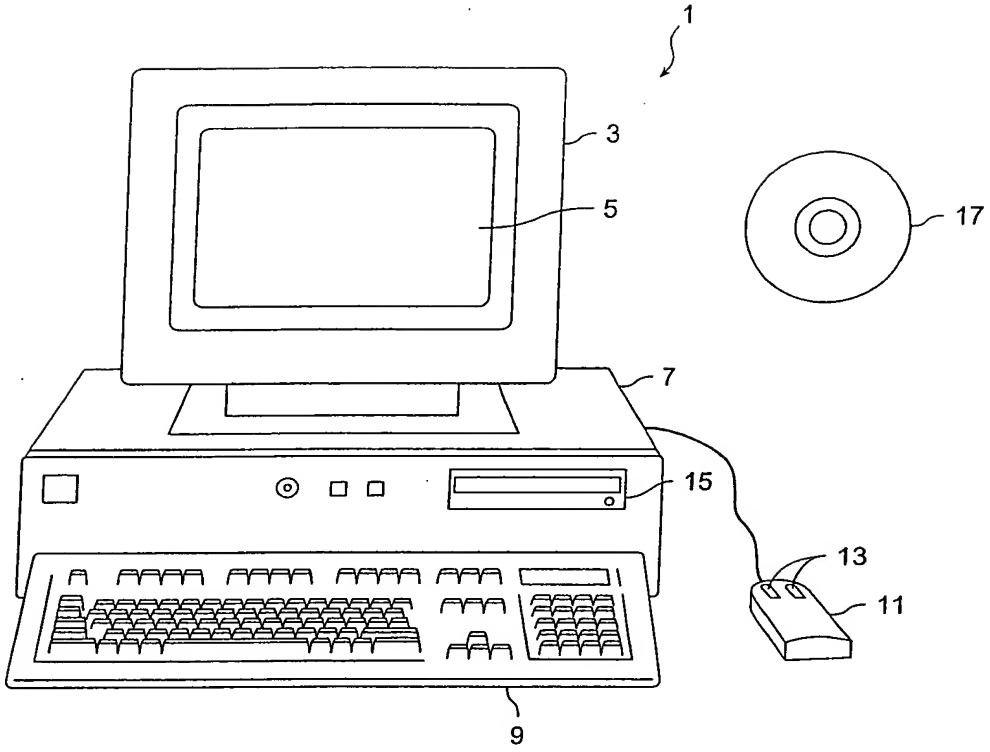

1
3
5
17
7
15
13
11
9

FIG. 5

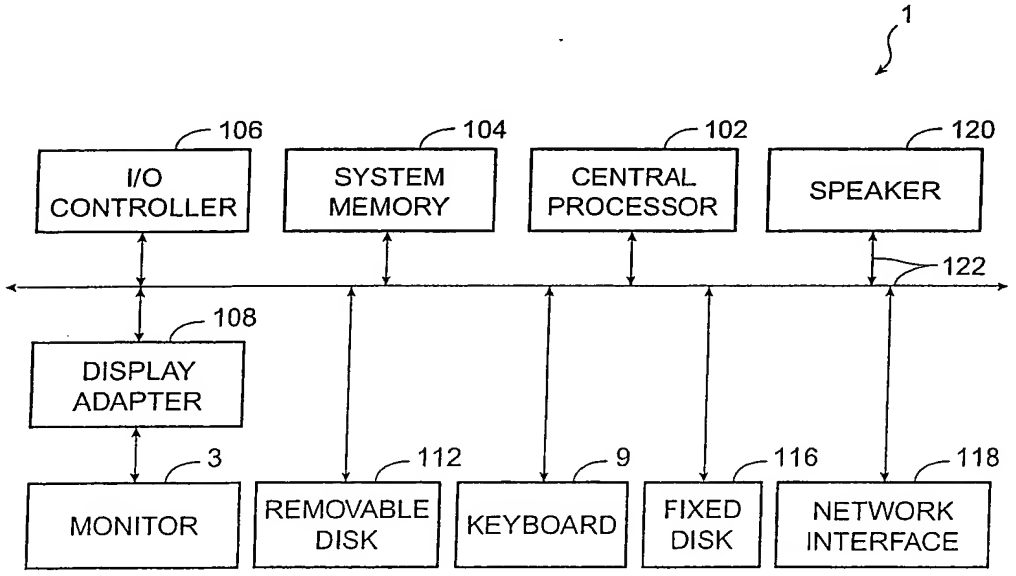

1
106
I/O CONTROLLER
104
SYSTEM MEMORY
102
CENTRAL PROCESSOR
120
SPEAKER
122
108
DISPLAY ADAPTER
3
MONITOR
112
REMOVABLE DISK
9
KEYBOARD
116
FIXED DISK
118
NETWORK INTERFACE

FIG. 6

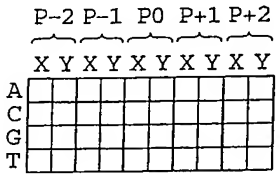


FIG. 7

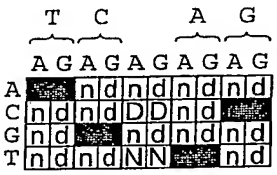


FIG. 8

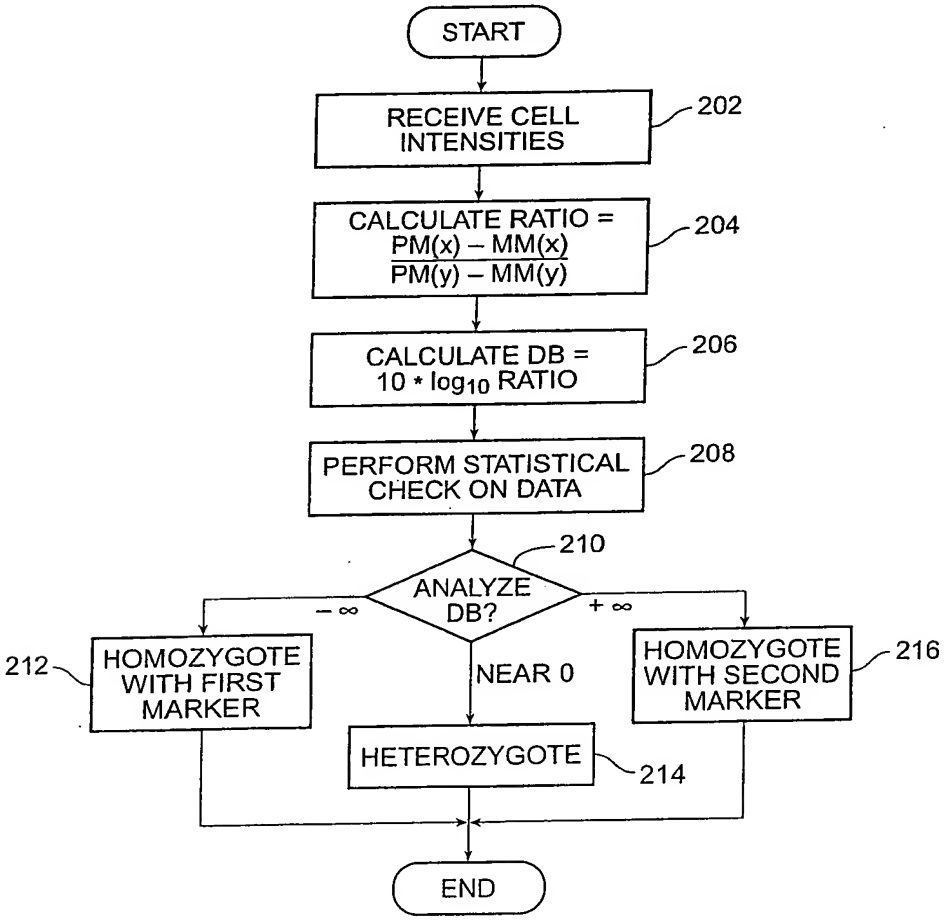


FIG. 9

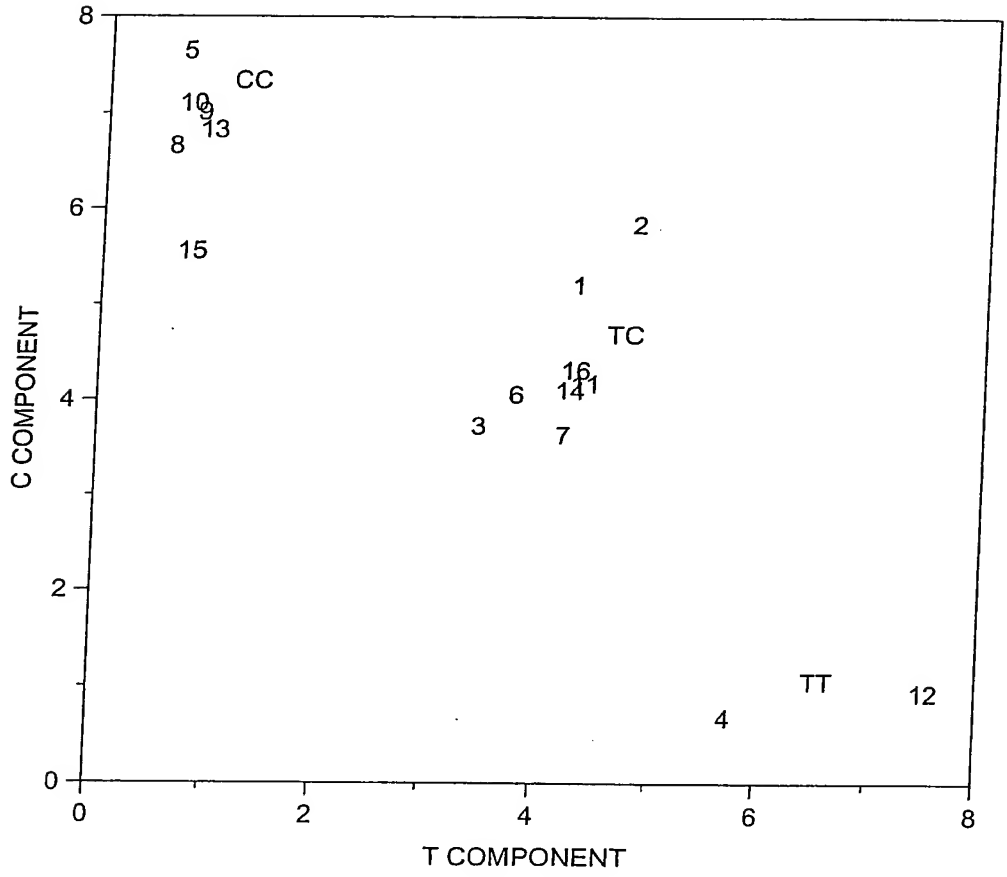

8
6
4
2
0
C COMPONENT
0
2
4
6
8
T COMPONENT
5
CC
10
9
13
8
15
2
1
TC
16
6
14
1
3
7
TT
12
4

FIG. 10

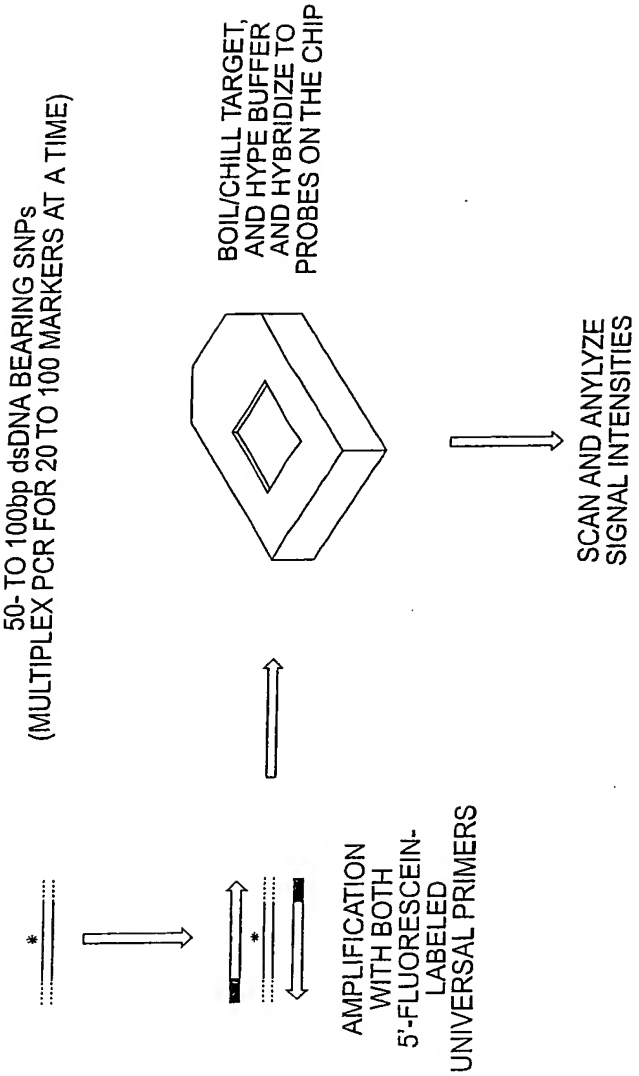

50- TO 100bp dsDNA BEARING SNPs
(MULTIPLEX PCR FOR 20 TO 100 MARKERS AT A TIME)
AMPLIFICATION WITH BOTH 5'-FLUORESCEIN-LABELED UNIVERSAL PRIMERS
BOIL/CHILL TARGET, AND HYPE BUFFER AND HYBRIDIZE TO PROBES ON THE CHIP
SCAN AND ANYLYZE SIGNAL INTENSITIES

FIG. 11

DB = "DECIBELS" = 10 X LOG (DETECTION RATIO)

DETECTION RATIO = $\frac{\text{A PERFECT MATCH} - \text{A MISMATCHES}}{\text{B PERFECT MATCH} - \text{B MISMATCHES}}$

C = SIGNIFICANCE CHECK = $\frac{\text{MAX (A OR B PERFECT MATCH)}}{\sigma\text{ (A OR B MISMATCHES)}} > 2$

P = PATTERN MATCHING = $\frac{\text{MEAN [MAX (A OR B PERFECT MATCHES)]}}{\text{MEAN [MAX(A OR B MISMATCHES)]}} > 1.2$

PREDICTED PATTERNS

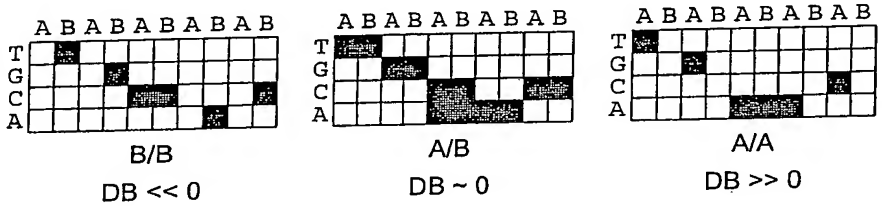


FIG. 12

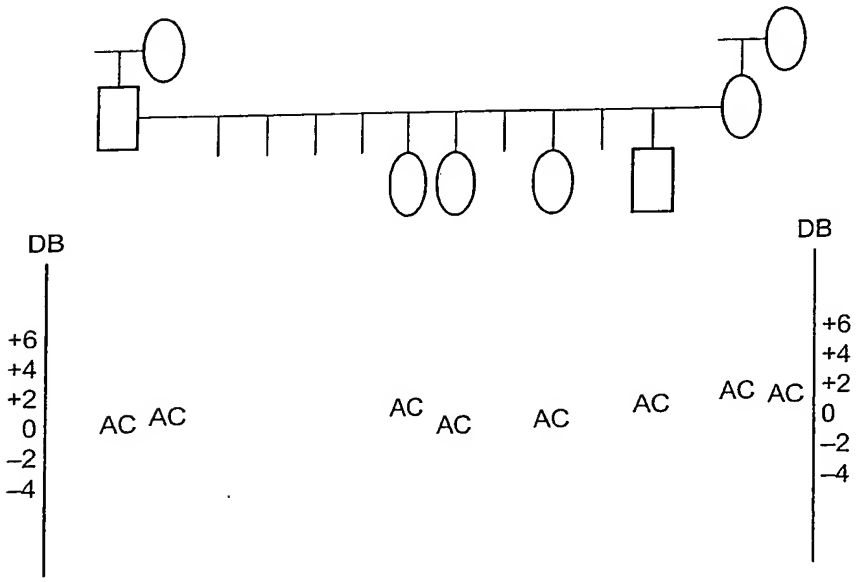


FIG. 13